MASTER PROJECT

Genomic evidence of local adaptation in spruce:
On the use of parallel clines.

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Keywords: population genetics, demography history, local adaptation, Norway spruce.

Background: Hybridization and introgression have both played a major role in the evolution of plant species. Contacts between species and the ensuing hybridization and introgression have often been associated to abrupt changes in environmental conditions. However, as (re)colonization implies abrupt environmental changes, selection and locally adapted species could also play a major role in the structure of the hybrid zones. In some cases, both processes might have facilitated the spread of species, for instance through the introgression of adaptive genomic regions from one genomic background to another. Disentangling the role selection from that of neutral processes in current species distribution and their consequences on genome evolution is challenging given the complexity of the population structure resulting from hybridization and introgression. Recent approaches, emphasizing the importance of the sampling design, consist in comparing two distinct species that diverged millions years ago but have since then be confronted to the same environmental gradient to identify loci underlying local adaptation. The current distribution of both P. abies and P. obovata allows us to follow a similar approach as they are both distributed along the same environmental gradients.

Seedlings collected in a set of P. abies, P. obovata and hybrid populations sampled across repeated environmental gradients (altitudinal, latitudinal and longitudinal) were grown in controlled conditions. Furthermore, 10 individuals per population (~30 populations) have been sequenced using exome capture (~800,000 SNPs). Is the current distribution the two species only the consequence of past population movements following the last glacial period or also the consequence of adaptation along environmental gradients with locally well adapted species?

Task and learning outcomes: The student will approach these questions through a combination of genomic and statistical analyzes to study the patterns of variation of genetic, phenotypic and environmental data.

- Inferential statistics on both climatic records and phenotypic data
- Phylogenetic analysis
- Population genetics analyses

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